

SEQUENCE LISTING

<110> Nandabalan, Krishnan
Yang, Meija

<120> p27(Kip-1)-FKBP-12 Protein Complexes

<130> Cura-14 US: p27(Kip-1)-FKBP-12 Complex

<140> 09/719,755

<141> 2000-12-15

<150> PCT/US99/13659

<151> 1999-06-18

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 597

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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 gac gcc agg cag gcg gag cac ccc aag ccc tcg gcc tgc agg aac ctc	96
Asp Ala Arg Gln Ala Glu His Pro Lys Pro Ser Ala Cys Arg Asn Leu	
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 ttc ggc ccg gtg gac cac gaa gag tta acc cgg gac ttg gag aag cac	144
Phe Gly Pro Val Asp His Glu Glu Leu Thr Arg Asp Leu Glu Lys His	
35 40 45	
 tgc aga gac atg gaa gag gcg agc cag cgc aag tgg aat ttc gat ttt	192
Cys Arg Asp Met Glu Glu Ala Ser Gln Arg Lys Trp Asn Phe Asp Phe	
50 55 60	
 cag aat cac aaa ccc cta gag ggc aag tac gag tgg caa gag gtg gag	240
Gln Asn His Lys Pro Leu Glu Gly Lys Tyr Glu Trp Gln Glu Val Glu	
65 70 75 80	

aag ggc agc ttg ccc gag ttc tac tac aga ccc ccg cgg ccc ccc aaa 288
 Lys Gly Ser Leu Pro Glu Phe Tyr Tyr Arg Pro Pro Arg Pro Pro Lys
 85 90 95

ggg gcc tgc aag gtg ccg gcg cag gag agc cag gat gtc agc ggg agc 336
 Gly Ala Cys Lys Val Pro Ala Gln Glu Ser Gln Asp Val Ser Gly Ser
 100 105 110

cgc ccg gcg gcg cct tta att ggg gct ccg gct aac tct gag gac acg 384
 Arg Pro Ala Ala Pro Leu Ile Gly Ala Pro Ala Asn Ser Glu Asp Thr
 115 120 125

cat ttg gtg gac cca aag act gat ccg tcg gac agc cag acg ggg tta 432
 His Leu Val Asp Pro Lys Thr Asp Pro Ser Asp Ser Gln Thr Gly Leu
 130 135 140

gcg gag caa tgc gca gga ata agg aag cga cct gca acc gac gat tct 480
 Ala Glu Gln Cys Ala Gly Ile Arg Lys Arg Pro Ala Thr Asp Asp Ser
 145 150 155 160

tct act caa aac aaa aga gcc aac aga aca gaa gaa aat gtt tca gac 528
 Ser Thr Gln Asn Lys Arg Ala Asn Arg Thr Glu Glu Asn Val Ser Asp
 165 170 175

ggg tcc cca aat gcc ggt tct gtg gag cag acg ccc aag aag cct ggc 576
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Phe Gly Pro Val Asp His Glu Glu Leu Thr Arg Asp Leu Glu Lys His
 35 40 45

Cys Arg Asp Met Glu Glu Ala Ser Gln Arg Lys Trp Asn Phe Asp Phe
 50 55 60
 Gln Asn His Lys Pro Leu Glu Gly Lys Tyr Glu Trp Gln Glu Val Glu
 65 70 75 80
 Lys Gly Ser Leu Pro Glu Phe Tyr Tyr Arg Pro Pro Arg Pro Pro Lys
 85 90 95
 Gly Ala Cys Lys Val Pro Ala Gln Glu Ser Gln Asp Val Ser Gly Ser
 100 105 110
 Arg Pro Ala Ala Pro Leu Ile Gly Ala Pro Ala Asn Ser Glu Asp Thr
 115 120 125
 His Leu Val Asp Pro Lys Thr Asp Pro Ser Asp Ser Gln Thr Gly Leu
 130 135 140
 Ala Glu Gln Cys Ala Gly Ile Arg Lys Arg Pro Ala Thr Asp Asp Ser
 145 150 155 160
 Ser Thr Gln Asn Lys Arg Ala Asn Arg Thr Glu Glu Asn Val Ser Asp
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 180 185 190
 Leu Arg Arg Arg Gln Thr
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Thr	Phe	Pro	Lys	Arg	Gly	Gln	Thr	Cys	Val	Val	His	Tyr	Thr	Gly	Met	
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ctt	gaa	gat	gga	aag	aaa	ttt	gat	tcc	tcc	cgg	gac	aga	aac	aag	ccc	147
Leu	Glu	Asp	Gly	Lys	Lys	Phe	Asp	Ser	Ser	Arg	Asp	Arg	Asn	Lys	Pro	
				35					40					45		

ttt	aag	ttt	atg	cta	ggc	aag	cag	gag	gtg	atc	cga	ggc	tgg	gaa	gaa	195
Phe	Lys	Phe	Met	Leu	Gly	Lys	Gln	Glu	Val	Ile	Arg	Gly	Trp	Glu	Glu	
			50					55					60			

ggg	gtt	gcc	cag	atg	agt	gtg	ggt	cag	aga	gcc	aaa	ctg	act	ata	tct	243
Gly	Val	Ala	Gln	Met	Ser	Val	Gly	Gln	Arg	Ala	Lys	Leu	Thr	Ile	Ser	
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cca	gat	tat	gcc	tat	ggt	gcc	act	ggg	cac	cca	ggc	atc	atc	cca	cca	291
Pro	Asp	Tyr	Ala	Tyr	Gly	Ala	Thr	Gly	His	Pro	Gly	Ile	Ile	Pro	Pro	
	80					85					90					

cat	gcc	act	ctc	gtc	ttc	gat	gtg	gag	ctt	cta	aaa	ctg	gaa			333
His	Ala	Thr	Leu	Val	Phe	Asp	Val	Glu	Leu	Leu	Lys	Leu	Glu			
	95				100				105							

tgacaggaat	ggcctcctcc	cttagctccc	tgttcttgga	tctgcctgga	gggatctggg	393
gcctccagac	atgtgcacat	gatccatatg	gagcttttcc	tgatgttcca	ctccactttg	453
tatagacatc	tgccctgact	gaatgtgttc	tgtcactcag	ctttgcttcc	gacacctctg	513
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 20 25 30
 Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
 35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
 50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
 65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
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Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu
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<220>
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<400> 6
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